

Single cell RNA-seq data due to Jaitin et al (2014), Deng et al (2014) and Zeisel et al (2015)

Kushal K Dey, Chiaowen Joyce Hsiao & Matthew Stephens

Stephens Lab, The University of Chicago

*Corresponding Email: mstephens@uchicago.edu

March 20, 2016

Abstract

We present three selected single cell RNA-seq data as *ExpressionSet* objects. These datasets include Mouse spleen single cell data due to Jaitin et al 2014 [1], Mouse embryonic stem cell data due to Deng et al 2014 [2] and Mouse cortex and hippocampus single cell data due to Zeisel et al 2015 [3]. **singlecellRNAseqData version: 0.99.0** ¹

¹This document used the vignette from *Bioconductor* package [DESeq2](#), [cellTree](#), [CountClust](#) as *knitr* template

Contents

1	Installation	2
2	Deng et al (2014)	2
3	Jaitin et al (2014)	4
4	Zeisel et al (2015)	5

1 Installation

To install the Bioconductor version of this package,

```
source("http://bioconductor.org/biocLite.R")
biocLite("singlecellRNAseqData")
```

To install the working version from Github, the user needs CRAN package [devtools](#).

```
library(devtools)
install_github("kkdey/singlecellRNAseqData")
```

To load the package

```
library(singlecellRNAseqData)
```

We now provide a brief summary of the three datasets hosted in this package and how the user can extract different features of the data from the *ExpressionSet* framework in which the data is stored.

2 Deng et al (2014)

Deng et al (2014) [2] collected embryonic stem cell (ESC) data from mouse spanning across several stages of mouse embryo development (zygote, 2 cell, 4 cell, 8 cell, 16 cell, early blastocyst, mid blastocyst and late blastocyst stages). We present the data for a filtered set of 259 ESCs (after removing SmartSeq and pooled samples) with reads measured across 22431 genes. The data has been processed from the data publicly available at Gene Expression Omnibus (GEO:GSE45719: see <http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE45719>)

```
data("Deng2014MouseESC")
Deng2014MouseESC

## ExpressionSet (storageMode: lockedEnvironment)
## assayData: 22431 features, 259 samples
##   element names: exprs
## protocolData: none
```

```
## phenoData
##   sampleNames: V278 V279 ... V205 (259 total)
##   varLabels: cell_type embryo_id
##   varMetadata: labelDescription
## featureData
##   featureNames: 0610005C13Rik 0610007C21Rik ... Zzz3 (22431 total)
##   fvarLabels: gene_name
##   fvarMetadata: labelDescription
## experimentData: use 'experimentData(object)'
## Annotation:
```

The expression data for the first few genes (along rows) and the first few cells in the sample (along columns)

```
exprs <- exprs(Deng2014MouseESC)
head(exprs[,1:5])

##           V278 V279 V280 V281 V115
## 0610005C13Rik    0    0    0    0    2
## 0610007C21Rik  194  148  378  208  26
## 0610007L01Rik 4940 5034 3714 2538 667
## 0610007P08Rik  323  672  226  241  219
## 0610007P14Rik 2501 3203 2467 1952 1195
## 0610007P22Rik   96  220  115  133   41
```

The phenotype or metadata on the samples includes the development stage of the cell and the embryo ID of the corresponding developing embryo. The development stage information can be extracted as follows

```
pdata <- pData(Deng2014MouseESC)
table(pdata$cell_type)

##
##      16cell      4cell      8cell early2cell earlyblast  late2cell  lateblast
##          50          14          28           8          43           10          30
##   mid2cell  midblast      zy
##          12          60          4
```

The gene names corresponding to the rows of the expression matrix can be extracted as follows

```
features <- featureNames(Deng2014MouseESC)
head(features)

## [1] "0610005C13Rik" "0610007C21Rik" "0610007L01Rik" "0610007P08Rik"
## [5] "0610007P14Rik" "0610007P22Rik"
```

3 Jaitin et al (2014)

Jaitin et al (2014) [1] collected single cell data from Mouse spleen using several sorting markers, with the purpose of decomposing tissues into cell types. Expression was recorded for 4590 samples of single cells with reads measured across 20190 genes. The data was processed from the publicly available data at Gene Expression Omnibus (GEO:GSE54006: see <http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE54006>)

```
data("MouseJaitinSpleen")
MouseJaitinSpleen

## ExpressionSet (storageMode: lockedEnvironment)
## assayData: 20190 features, 4590 samples
##   element names: exprs
## protocolData: none
## phenoData
##   sampleNames: 7 8 ... 4604 (4590 total)
##   varLabels: index sequencing_batch ...
##     Column_name_in_processed_data_file (15 total)
##   varMetadata: labelDescription
## featureData
##   featureNames: 0610007C21Rik_Apr3 0610007L01Rik ... ERCC-00002 (20190
##     total)
##   fvarLabels: gene_names
##   fvarMetadata: labelDescription
## experimentData: use 'experimentData(object)'
## Annotation:
```

The expression data for the first few genes (along rows) and the first few cells in the sample (along columns)

```
exprs <- exprs(MouseJaitinSpleen)
head(exprs[,1:5])

##           7 8 9 10 11
## 0610007C21Rik_Apr3 0 0 0 1 0
## 0610007L01Rik      0 1 0 0 0
## 0610007P08Rik      0 0 0 0 0
## 0610007P14Rik      0 1 0 0 0
## 0610007P22Rik      0 0 0 0 0
## 0610009B22Rik      0 0 0 0 0
```

Metadata is available on 15 features of the samples or single cells, including mouse ID, well ID, amplification batch, sequencing batch, ERCC features etc. The user can extract the sample metadata of interest as follows.

```
pdata <- pData(MouseJaitinSpleen)
head(pdata[,c("amplification_batch", "sorting_markers", "well_id", "ERCC_dilution")])
```

	amplification_batch	sorting_markers	well_id	ERCC_dilution
## 7	0	CD11c+	A1	2.00E-05
## 8	0	CD11c+	B1	2.00E-05
## 9	0	CD11c+	C1	2.00E-05
## 10	0	CD11c+	D1	2.00E-05
## 11	0	CD11c+	E1	2.00E-05
## 12	0	CD11c+	F1	2.00E-05

The gene names corresponding to the rows of the expression matrix can be extracted as follows

```
features <- featureNames(MouseJaitinSpleen)
head(features)
```

## [1]	"0610007C21Rik_Apr3"	"0610007L01Rik"	"0610007P08Rik"
## [4]	"0610007P14Rik"	"0610007P22Rik"	"0610009B22Rik"

4 Zeisel et al (2015)

Zeisel et al (2015) [3] collected single cell data from Mouse cortex and hippocampus, with the idea of identifying different cell types. Expression was recorded for 3005 samples of single cells with reads measured across 19968 genes. The data was processed from the publicly available data at Gene Expression Omnibus (GEO:GSE60361: see <http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE60361>)

```
data("MouseZeiselBrain")
MouseZeiselBrain
```

```
## ExpressionSet (storageMode: lockedEnvironment)
## assayData: 19968 features, 3005 samples
## element names: exprs
## protocolData: none
## phenoData
## sampleNames: 1772071015_C02 1772071017_G12 ... 1772058148_F03 (3005
## total)
## varLabels: tissue group_no ... level2_class (10 total)
## varMetadata: labelDescription
## featureData
## featureNames: Tspan12 Tshz1 ... Gm20738_loc3 (19968 total)
## fvarLabels: gene_name
## fvarMetadata: labelDescription
## experimentData: use 'experimentData(object)'
## Annotation:
```

The expression data for the first few genes (along rows) and the first few cells in the sample (along

columns)

```
exprs <- exprs(MouseZeiselBrain)
head(exprs[,1:5])
```

##	1772071015_C02	1772071017_G12	1772071017_A05	1772071014_B06
## Tspan12	0	0	0	3
## Tshz1	3	1	0	2
## Fnbp11	3	1	6	4
## Adamts15	0	0	0	0
## Cldn12	1	1	1	0
## Rxfp1	0	0	0	0
##	1772067065_H06			
## Tspan12	0			
## Tshz1	2			
## Fnbp11	1			
## Adamts15	0			
## Cldn12	0			
## Rxfp1	0			

Metadata is available on 10 features of the samples or single cells, including tissue of origin, class type of cells, age and sex of subjects from whom the cells were extracted.

```
pdata <- pData(MouseZeiselBrain)
head(pdata[,c("tissue", "sex", "age", "level1_class", "level2_class")])
```

##		tissue	sex	age	level1_class	level2_class
##	1772071015_C02	ssscortex	female	21	interneurons	Int10
##	1772071017_G12	ssscortex	male	20	interneurons	Int10
##	1772071017_A05	ssscortex	male	20	interneurons	Int6
##	1772071014_B06	ssscortex	female	21	interneurons	Int10
##	1772067065_H06	ssscortex	female	25	interneurons	Int9
##	1772071017_E02	ssscortex	male	20	interneurons	Int9

The gene names corresponding to the rows of the expression matrix can be extracted as follows

```
features <- featureNames(MouseZeiselBrain)
head(features)
```

##	[1]	"Tspan12"	"Tshz1"	"Fnbp11"	"Adamts15"	"Cldn12"	"Rxfp1"

References

- [1] Jaitin DA, Kenigsberg E et al. Massively Parallel Single-Cell RNA-Seq for Marker-Free Decomposition of Tissues into Cell Types. *Science*. 343 (6172) 776-779, 2014. DOI: 10.1126/science.1247651

- [2] Deng Q, Ramskold D, Reinius B, Sandberg R. Single-Cell RNA-Seq Reveals Dynamic, Random Monoallelic Gene Expression in Mammalian Cells. *Science*. 343 (6167) 193-196, 2014. DOI: 10.1126/science.1245316
- [3] Zeisel A, Munoz-Manchado AB, Codeluppi S *et al*. Cell types in the mouse cortex and hippocampus revealed by single-cell RNA-seq. *Science*. 34: 6226, 1138-1142, 2015. DOI:10.1126/science.aaa1934